

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is primate DIRS1 nucleotide sequence.
SEQ ID NO: 2 is primate DIRS1 polypeptide sequence.
SEQ ID NO: 3 is primate DIRS2 nucleotide sequence.
SEQ ID NO: 4 is primate DIRS2 polypeptide sequence.
SEQ ID NO: 5 is primate IFN γ receptor subunit beta polypeptide sequence.
10 SEQ ID NO: 6 is primate CRF2-4 receptor subunit polypeptide sequence.

(1) GENERAL INFORMATION:

15 (i) APPLICANT: Parham, Christi L.
Moore, Kevin W.
Murgolo, Nicholas J.
Bazan, J. Fernando

20 (ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related
Reagents and Methods

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

25 (A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
30 (F) ZIP: 94304-1104

35 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

40 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 08-MAR-1999
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Ching, Edwin P.
 (B) REGISTRATION NUMBER: 34,090
 (C) REFERENCE/DOCKET NUMBER: DX0804K

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1381 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
10 (A) NAME/KEY: CDS
(B) LOCATION: 132..1064

(ix) FEATURE:
15 (A) NAME/KEY: misc_feature
(B) LOCATION: 567
(D) OTHER INFORMATION: /note= "nucleotides 567, 573, 1336, 1342, and 1369 designated C, but each may be A, C, G, or T"

(ix) FEATURE:
20 (A) NAME/KEY: misc_feature
(B) LOCATION: 643
(D) OTHER INFORMATION: /note= "nucleotides 643, 1287, and 1290 designated C, but each may be C or G"

(ix) FEATURE:
25 (A) NAME/KEY: misc_feature
(B) LOCATION: 772
(D) OTHER INFORMATION: /note= "nucleotides 772, 806, and 1261 designated G, but each may be A or G"

(ix) FEATURE:
30 (A) NAME/KEY: misc_feature
(B) LOCATION: 1236
(D) OTHER INFORMATION: /note= "nucleotides 1236, 1260, 1282, and 1289 are designated T, but each may be G or T"

(ix) FEATURE:
35 (A) NAME/KEY: misc_feature
(B) LOCATION: 1247
(D) OTHER INFORMATION: /note= "nucleotides 1247, 1257, 1293, and 1302 designated C, but each may be C or T"

(ix) FEATURE:
40 (A) NAME/KEY: misc_feature
(B) LOCATION: 1266
(D) OTHER INFORMATION: /note= "nucleotides 1266 and 1298 designated T, but each may be A or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
50 TCGACCCACG CGTCCGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA 60
AGATGGCTGA GATGGACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAAC 120
55 GAGTCTACCA A ATG CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA 170

Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
1 5 10

5	AGT CTT TTC ATG TGG TTT TTC TAC GCA TTG ATT CCA TGT TTG CTC ACA	218
	Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr	
	15 20 25	
10	GAT GAA GTG GCC ATT CTG CCT GCC CCT CAG AAC CTC TCT GTA CTC TCA	266
	Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	
	30 35 40 45	
15	ACC AAC ATG AAG CAT CTC TTG ATG TGG AGC CCA GTG ATC GCG CCT GGA	314
	Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly	
	50 55 60	
20	GAA ACA GTG TAC TAT TCT GTC GAA TAC CAG GGG GAG TAC GAG AGC CTG	362
	Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu	
	65 70 75	
25	TAC ACG AGC CAC ATC TGG ATC CCC AGC AGC TGG TGC TCA CTC ACT GAA	410
	Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu	
	80 85 90	
30	GGT CCT GAG TGT GAT GTC ACT GAT GAC ATC ACG GCC ACT GTG CCA TAC	458
	Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr	
	95 100 105	
35	AAC CTT CGT GTC AGG GCC ACA TTG GGC TCA CAG ACC TCA GCC TGG AGC	506
	Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser	
	110 115 120 125	
40	ATC CTG AAG CAT CCC TTT AAT AGA AAC TCA ACC ATC CTT ACC CGA CCT	554
	Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro	
	130 135 140	
45	GGG ATG GAG ATC CCC AAA CAT GGC TTC CAC CTG GTT ATT GAG CTG GAG	602
	Gly Met Glu Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu	
	145 150 155	
50	GAC CTG GGG CCC CAG TTT GAG TTC CTT GTG GCC TAC TGG ACG AGG GAG	650
	Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu	
	160 165 170	
55	CCT GGT GCC GAG GAA CAT GTC AAA ATG GTG AGG AGT GGG GGT ATT CCA	698
	Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro	
	175 180 185	
60	GTG CAC CTA GAA ACC ATG GAG CCA GGG GCT GCA TAC TGT GTG AAG GCC	746
	Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala	
	190 195 200 205	
65	CAG ACA TTC GTG AAG GCC ATT GGG AGG TAC AGC GCC TTC AGC CAG ACA	794
	Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr	
	210 215 220	

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	GAA TGT GTG GAG GTG CAA GGA GAG GCC ATT CCC CTG GTA CTG GCC CTG	842
	Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu	
	225 230 235	
5	TTT GCC TTT GTT GGC TTC ATG CTG ATC CTT GTG GTC GTG CCA CTG TTC	890
	Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe	
	240 245 250	
10	GTC TGG AAA ATG GGC CGG CTG CTC CAG TAC TCC TGT TGC CCC GTG GTG	938
	Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val	
	255 260 265	
15	GTC CTC CCA GAC ACC TTG AAA ATA ACC AAT TCA CCC CAG AAG TTA ATC	986
	Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	
	270 275 280 285	
20	AGC TGC AGA AGG GAG GAG GTG GAT GCC TGT GCC ACG GCT GTG ATG TCT	1034
	Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser	
	290 295 300	
	CCT GAG GAA CTC CTC AGG GCC TGG ATC TCA TAGGTTTGCG GAAGGGCCCA	1084
	Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	
	305 310	
25	GGTGAAGCCG AGAACCTGGT CTGCATGACA TGGAAACCAT GAGGGGACAA GTTGTGTTTC	1144
	TGTTTTCCGC CACGGACAAG GGATGAGAGA AGTAGGAAGA GCCTGTTGTC TACAAGTCTA	1204
30	GAAGCAACCA TCAGAGGCAG GGTGGTTTGT CTAACAGAAC AACTGACTGA GGCTATGGGG	1264
	GTTGTGACCT CTAGACTTTG GGCTTCCACT TGCTTGGCTG AGCAACCCTG GGAAAAGTGA	1324
	CTTCATCCCT TCGGTCCCAA GTTTTCTCAT CTGTAATGGG GGATCCCTAC AAAACTG	1381
35	(2) INFORMATION FOR SEQ ID NO:2:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 311 amino acids	
	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
	Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe	
	1 5 10 15	
50	Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val	
	20 25 30	
	Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met	
55	35 40 45	

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Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 50 55 60
 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 5 65 70 75 80
 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 85 90 95
 10 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 100 105 110
 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 115 120 125
 15 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 130 135 140
 Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 20 145 150 155 160
 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu Pro Gly Ala
 165 170 175
 25 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 180 185 190
 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 195 200 205
 30 Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 210 215 220
 Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 35 225 230 235 240
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 245 250 255
 40 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 260 265 270
 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 275 280 285
 45 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 290 295 300
 Leu Leu Arg Ala Trp Ile Ser
 50 305 310

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1244 base pairs

668060-04559260

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS
(B) LOCATION: 2..694

(ix) FEATURE:

15 (A) NAME/KEY: misc_feature
(B) LOCATION: 193
(D) OTHER INFORMATION: /note= "nucleotide 193 designated
C, may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	C CGG GTC GAC CCA CGC GTC CGC CTG GTT TCC CCC TGG CTG ACA GTG Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val	46
	1 5 10 15	
25	CCT TGG TTC CTG TCC TGT TGG AAT GTT ACC ATT GGG CCT CCT GAG AGC Pro Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser	94
	20 25 30	
30	ATC TGG GTG ACG CCG GGA GAA GCC TCC CTC ATC ATC AGG TTC TCC TCT Ile Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser	142
	35 40 45	
35	CCC TTC GAC GTC CCT CCC AAC CTG GGC TAT TTC CAG TAC TAT GTC CAT Pro Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His	190
	50 55 60	
40	TAC TGG GAA AAG GCG GGA ATC CAA AAG GTT AAA GGT CCT TTC AAG AGC Tyr Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser	238
	65 70 75	
45	AAC TCC ATC GTG TTG GAT GGC TTG AGA CCC TTA AGA GAA TAC TGT TTA Asn Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu	286
	80 85 90 95	
50	CAA GTG AAG GCG CAT CTC TTT CGC ACA TCC TGC AAC ACC TCT AGG CCC Gln Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro	334
	100 105 110	
55	GGC CGC TTA AGC AAC ATA ACT TGC TAC GAA ACA ATG ATG GAT GCC ACT Gly Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr	382
	115 120 125	
60	ACG AAG CTT CAA CAA GTC ATC CTC ATC GCC GTG GGA GTC TTT CTG TCG Thr Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser	430
	130 135 140	

CTG GCG GCG CTG GCG GGG GGC TGT TTC TTC CTG GTG CTG AGA TAC AAA 478
Leu Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys
145 150 155

5 GGC CTG GTG AAA TAC TGG TTT CAC TCT CCG CCA AGC ATC CCA TCA CAA 526
Gly Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln
160 165 170 175

10 ATC GAA GAG TAT CTG AAG GAC CCG AGC CAG CCT ATC CTA GAG GCC CTG 574
Ile Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu
180 185 190

15 GAC AAG GAC ACG TCA CCA ACA GAT GAT GCC TGG GAC TTG GTG TCT GTT 622
Asp Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val
195 200 205

20 GTT GCA TTT CCA GCA AAG GAG CAA GAA GAT GTT CCC CAA AGC ACT TTG 670
Val Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu
210 215 220

25 ACC CAA AAC TCT GGT GCG GTC TGC TAGCCTGTGG GGTAAGGGCT CTGAGCCGAG 724
Thr Gln Asn Ser Gly Ala Val Cys
225 230

GAAGCTGCTG ATGTCCATGT CAGCACTTTA TGGAATCCGG TCCTCCATTT TCCTGTCCCC 784

AAAAGGCCCG TCAGTGCCTG TGAAGATGTA ACGGGTCTCA TGGGGGCGAC AAGCTTATTG 844

30 ATTTTTTTTCT TCAAACATAAG AGTTTTCTAA TCATACGCGT TTTTAGAATA ATTCTACAGA 904

TATGTCCCCG AAAGATTAAG ATTTCTCTTA AACACTAAAA AGACATGTAA TTATTTGTTA 964

35 GCAAATGGGC GTCTGGCACG CCTCTGACAC TTTTTCGTCA GCAGCCAGGA CACGAGGTCC 1024

CCTCCTTGAT GAAGCCCCTC GGGCAGACCA TGTCACCTGT CCCAGCCTGC CCCAAGAAGG 1084

GACATTAAGT GGCCCTTCTT CATATCCAAA CACCTGGCTT GAAATGTGAT TAGCCCTGTA 1144

40 AATAGTTTCA CAGAGATTAA GCCTTTTTTTT CCCCCAAGTT AGGAATAAAA GACTATAATT 1204

AACTTTTTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1244

45 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

55

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

SECRET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Leu Gly Val Phe
1 5 10 15

10 Ala Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
35 40 45

15 Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg
50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
65 70 75 80

20 Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
85 90 95

25 Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
115 120 125

30 Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
145 150 155 160

35 Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
165 170 175

40 Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
195 200 205

45 Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
225 230 235 240

50 Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
245 250 255

55 Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
260 265 270

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
115 120 125

NAME	AGE	SEX	REL	EDUC	INDUSTRY	STATUS	REMARKS
John Doe	35	M	H	HS	Farmer	W	Good
Jane Doe	32	F	W	HS	Homemaker	W	Good
Robert Smith	45	M	H	HS	Teacher	W	Good
Mary Smith	42	F	W	HS	Homemaker	W	Good
William Brown	55	M	H	HS	Retired	W	Good
Elizabeth Brown	52	F	W	HS	Homemaker	W	Good
James Wilson	60	M	H	HS	Retired	W	Good
Patricia Wilson	58	F	W	HS	Homemaker	W	Good
Charles Davis	70	M	H	HS	Retired	W	Good
Barbara Davis	68	F	W	HS	Homemaker	W	Good
Thomas Miller	75	M	H	HS	Retired	W	Good
Linda Miller	72	F	W	HS	Homemaker	W	Good
Richard Moore	80	M	H	HS	Retired	W	Good
Susan Moore	78	F	W	HS	Homemaker	W	Good

	Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
	130						135					140					
5	Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
	145					150					155					160	
	Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
					165					170					175		
10	Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
				180					185					190			
	Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
			195					200					205				
15	Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser	Trp	Met	Val	Ala	
	210						215					220					
	Val	Ile	Leu	Met	Ala	Ser	Val	Phe	Met	Val	Cys	Leu	Ala	Leu	Leu	Gly	
20	225					230					235					240	
	Cys	Phe	Ser	Leu	Leu	Trp	Cys	Val	Tyr	Lys	Lys	Thr	Lys	Tyr	Ala	Phe	
				245						250					255		
25	Ser	Pro	Arg	Asn	Ser	Leu	Pro	Gln	His	Leu	Lys	Glu	Phe	Leu	Gly	His	
				260					265					270			
	Pro	His	His	Asn	Thr	Leu	Leu	Phe	Phe	Ser	Phe	Pro	Leu	Ser	Asp	Glu	
			275					280					285				
30	Asn	Asp	Val	Phe	Asp	Lys	Leu	Ser	Val	Ile	Ala	Glu	Asp	Ser	Glu	Ser	
	290						295					300					
	Gly	Lys	Gln	Asn	Pro	Gly	Asp	Ser	Cys	Ser	Leu	Gly	Thr	Pro	Pro	Gly	
35	305					310					315					320	
	Gln	Gly	Pro	Gln	Ser												
					325												

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